

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: O'Brien, John S.
- (ii) TITLE OF THE INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/928,074
 - (B) FILING DATE: 11-SEP-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/611,307
 - (B) FILING DATE: 05-MAR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/04143
 - (B) FILING DATE: 05-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Haile, Ph.D., Lisa A.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 07256/024001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619/678-5070
 - (B) TELEFAX: 619/678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Met Thr Lys Leu I

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2...2

(D) OTHER INFORMATION: Ala at position 2 is a D-enantiomer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Ala Leu Ile Asp Asn Asn Ala Thr Glu Glu Ile Leu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Gln Phe Val Met Asn Lys Phe Ser Glu Leu Ile Val Asn Asn Ala
1 5 10 15
Thr Glu Glu Leu Leu Tyr
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Gln Leu Val Asn Arg Lys Leu Ser Glu Leu Ile Ile Asn Asn Ala
1 5 10 15
Thr Glu Glu Leu Leu
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Glu Tyr Val Val Lys Lys Val Met Leu Leu Ile Asp Asn Asn Arg
1 5 10 15
Thr Glu Glu Lys Ile Ile
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Glu Phe Val Val Lys Glu Val Ala Lys Leu Ile Asp Asn Asn Arg
1 5 10 15
Thr Glu Glu Glu Ile Leu
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asp Asn Lys
1 5 10 15
Thr Glu Lys Glu Ile Leu
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Lys Leu Ile Asp Asn Asp Lys Thr Glu Lys Glu Ile Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Lys Ser Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Val Lys His Gln Gly Leu Asn Lys Asn Ile Asn Leu Asp Ser Val
1 5 10 15
Asp Gly Val Pro
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
1 5 10 15
Thr

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
1 5 10 15
Val

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys
1 5 10 15
Ala Pro

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Pro Asn Ile Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu
1 5 10 15
Leu

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
1 5 10 15
Ile Leu

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGT GAA TTC CTG GTG AAG GAG GTG ACC AAG CTG ATT GAC AAC AAC AAG
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
1 5 10 15

48

ACT GAG AAA GAA ATA CTC
Thr Glu Lys Glu Ile Leu
20

66

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG TAC GCC CTC TTC CTC CTG GCC AGC CTC CTG GGC GCG GCT CTA GCC
Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
1 5 10 15

48

GGC CCG GTC CTT GGA CTG AAA GAA TGC ACC AGG GGC TCG GCA GTG TGG
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
20 25 30

96

TGC CAG AAT GTG AAG ACG GCG TCC GAC TGC GGG GCA GTG AAG CAC TGC
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
35 40 45

144

CTG CAG ACC GTT TGG AAC AAG CCA ACA GTG AAA TCC CTT CCC TGC GAC
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
50 55 60

192

ATA TGC AAA GAC GTT GTC ACC GCA GCT GGT GAT ATG CTG AAG GAC AAT
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65 70 75 80

240

GCC ACT GAG GAG GAG ATC CTT GTT TAC TTG GAG AAG ACC TGT GAC TGG
Ala Thr Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
85 90 95

288

CTT CCG AAA CCG AAC ATG TCT GCT TCA TGC AAG GAG ATA GTG GAC TCC
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
100 105 110

336

TAC CTC CCT GTC ATC CTG GAC ATC ATT AAA GGA GAA ATG AGC CGT CCT
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
115 120 125

384

GGG GAG GTG TGC TCT GCT CTC AAC CTC TGC GAG TCT CTC CAG AAG CAC
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
130 135 140

432

CTA GCA GAG CTG AAT CAC CAG AAG CAG CTG GAG TCC AAT AAG ATC CCA Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro 145 150 155 160	480
GAG CTG GAC ATG ACT GAG GTG GTG GCC CCC TTC ATG GCC AAC ATC CCT Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro 165 170 175	528
CTC CTC CTC TAC CCT CAG GAC GGC CCC CGC AGC AAG CCC CAG CCA AAG Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys 180 185 190	576
GAT AAT GGG GAC GTT TGC CAG GAC TGC ATT CAG ATG GTG ACT GAC ATC Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile 195 200 205	624
CAG ACT GCT GTA CGG ACC AAC TCC ACC TTT GTC CAG GCC TTG GTG GAA Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu 210 215 220	672
CAT GTC AAG GAG GAG TGT GAC CGC CTG GGC CCT GGC ATG GCC GAC ATA His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile 225 230 235 240	720
TGC AAG AAC TAT ATC AGC CAG TAT TCT GAA ATT GCT ATC CAG ATG ATG Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met 245 250 255	768
ATG CAC ATG CAA CCC AAG GAG ATC TGT GCG CTG GTT GGG TTC TGT GAT Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp 260 265 270	816
GAG GTG AAA GAG ATG CCC ATG CAG ACT CTG GTC CCC GCC AAA GTG GCC Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala 275 280 285	864
TCC AAG AAT GTC ATC CCT GCC CTG GAA CTG GTG GAG CCC ATT AAG AAG Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys 290 295 300	912
CAC GAG GTC CCA GCA AAG TCT GAT GTT TAC TGT GAG GTG TGT GAA TTC His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe 305 310 315 320	960
CTG GTG AAG GAG GTG ACC AAG CTG ATT GAC AAC AAC AAG ACT GAG AAA Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys 325 330 335	1008
GAA ATA CTC GAC GCT TTT GAC AAA ATG TGC TCG AAG CTG CCG AAG TCC Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser 340 345 350	1056
CTG TCG GAA GAG TGC CAG GAG GTG GTG GAC ACG TAC GGC AGC TCC ATC Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile 355 360 365	1104
CTG TCC ATC CTG CTG GAG GAG GTC AGC CCT GAG CTG GTG TGC AGC ATG Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met 370 375 380	1152
CTG CAC CTC TGC TCT GGC ACG CGG CTG CCT GCA CTG ACC GTT CAC GTG Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val 385 390 395 400	1200

ACT CAG CCA AAG GAC GGT GGC TTC TGC GAA GTG TGC AAG AAG CTG GTG	1248
Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val	410 415
GGT TAT TTG GAT CGC AAC CTG GAG AAA AAC AGC ACC AAG CAG GAG ATC	1296
Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile	420 425 430
CTG GCT GCT CTT GAG AAA GGC TGC AGC TTC CTG CCA GAC CCT TAC CAG	1344
Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln	435 440 445
AAG CAG TGT GAT CAG TTT GTG GCA GAG TAC GAG CCC GTG CTG ATC GAG	1392
Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu	450 455 460
ATC CTG GTG GAG GTG ATG GAT CCT TCC TTC GTG TGC TTG AAA ATT GGA	1440
Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly	465 470 475 480
GCC TGC CCC TCG GCC CAT AAG CCC TTG TTG GGA ACT GAG AAG TGT ATA	1488
Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile	485 490 495
TGG GGC CCA AGC TAC TGG TGC CAG AAC ACA GAG ACA GCA GCC CAG TGC	1536
Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys	500 505 510
AAT GCT GTC GAG CAT TGC AAA CGC CAT GTG TGG AAC TAGGAGGAGG AATATT	1588
Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn	515 520
CCATCTTGGC AGAAACCACA GCATTGGTTT TTTTCTACTT GTGTGTCTGG GGAATGAAC	1648
GCACAGATCT GTTTGACTTT GTTATAAAAA TAGGGCTCCC CCACCTCCCC CATTCTGTG	1708
TCCTTTATTG TAGCATTGCT GTCTGCAAGG GAGCCCCTAG CCCCTGGCAG ACATAGCTGC	1768
TTCAGTGCCC CTTTCTCTCT TGCTAGATGG ATGTTGATGC ACTGGAGGTC TTTTAGCCTG	1828
CCCTTGTCATG GCGCCTGCTG GAGGAGGAGA GAGCTCTGCT GGCATGAGCC ACAGTTTCTT	1888
GACTGGAGGC CATCAACCCT CTTGGTTGAG GCCTGTCTCT GGCCTGACA TGTGCTTGGG	1948
CACTGGTGGG CCTGGGCTTC TGAGGTGGCC TCCTGCCCTG ATCAGGGACC CTCCCCGCTT	2008
TCCTGGGCCT CTCAGTTGAA CAAAGCAGCA AAACAAAGGC AGTTTATAT GAAAGATTAG	2068
AAGCCTGGAA TAATCAGGCT TTTTAAATGA TGTAATTCCT ACTGTAATAG CATAGGGATT	2128
TTGGAAGCAG CTGCTGGTGG CTTGGGACAT CAGTGGGGCC AAGGGTTCTC TGTCCCTGGT	2188
TCAACTGTGA TTTGGCTTTC CCGTGTCTTT CCTGGTGATG CCTGTTTGG GGTCTGTGG	2248
GTTTGGGTGG GAAGAGGGCA ATCTGCCTGA ATGTAACCTG CTAGCTCTCC GAAGGCCCTG	2308
CGGGCCTGGC TTGTGTGAGC GTGTGGACAG TGGTGGCCGC GCTGTGCCTG CTCGTGTTGC	2368
CTACATGTCC CTGGCTGTTG AGGCGCTGCT TCAGCCTGCA CCCCTCCCTT GTCTCATAGA	2428
TGCTCCTTTT GACCTTTTCA AATAAATATG GATGGCGAGC TCCTAGGCCT CTGGCTTCCT	2488
GGTAGAGGGC GGCATGCCGA AGGGTCTGCT CCGTGTGGAT TGGATGCTGG GGTGTGGGGG	2548
TTGGAAGCTG TCTGTGGCCC ACTTGGGCAC ACTTGGGCAC CCACGCTTCT GTCCACTTCT	2608
GGTTGCCAGG AGACAGCAAG CAAAGCCAGC AGGACATGAA GTTGCTATTA AATGGACTTC	2668
GTGATTTTGG TTTTGCACTA AAGTTTCTGT GATTTAACAA TAAATTCTG TTAGCCAGAA	2728
AAAAAAAAA AAAAAAAAAA A	2749

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
1 5 10 15
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
20 25 30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
35 40 45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
50 55 60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65 70 75 80
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
85 90 95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
100 105 110
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
115 120 125
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
130 135 140
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
145 150 155 160
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
165 170 175
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
180 185 190
Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
195 200 205
Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
210 215 220
His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
225 230 235 240
Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
245 250 255
Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp
260 265 270
Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala
275 280 285
Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys
290 295 300
His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe
305 310 315 320
Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys
325 330 335
Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser
340 345 350
Leu Ser Glu Glu Cys Gln Glu Val Asp Thr Tyr Gly Ser Ser Ile
355 360 365
Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met
370 375 380
Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val
385 390 395 400
Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val
405 410 415
Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile
420 425 430
Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln
435 440 445
Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu
450 455 460
Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly
465 470 475 480
Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile
485 490 495

Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys
 500 505 510
 Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn
 515 520

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr
 1 5 10 15
 Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe
 20 25 30
 Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln
 35 40 45
 Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu
 50 55 60
 Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly
 65 70 75 80